

1 TCGCGGCGGC CGTGATGGCT GGTGACGGCG GGGCCGGGCA GGGGACCGGG
51 GCCCGGGCCC GGGAGCGGGC CAGCTGCCGG GAGCCCTGAA TCACCGCCTG
101 GCCCCACTCC ACCATGAACG TCGCGCTGCA GGAGCTGGGA GCTGGCAGCA
151 ACATGGTGGA GTACAAACGGG GCCACGCTTC GGGATGAAGA CGCACCCGAG
201 ACCCCCCTAG AGGGCGGGC CTCCCCGGAC GCCATGGAGG TGGGCAAGGG
251 GGCTCCCT TTCTCACAG GCCCCAGCCC TGGCATGACG CCTGGCACAC
301 CCAGGAGCTC TGGGCTGTT TGGAGGGTCA CCTGCCCCCA CCTCCGCTCC
351 ATCTCTGGCC TCTGCTCTAG GACTATGGTG GGATTCCAGA AGGGGACAAG
401 ACAGCTGTTA GGCTCACGCA CGCAGCTGGA GCTGGTCTTA GCAGGTGCC
451 CTCTACTGCT GGCTGCACTG CTTCTGGGCT GCCTTGTGGC CCTAGGGGTC
501 CAGTACCAACA GAGACCCATC CCACAGCACC TGCCCTACAG AGGCCTGCAT
551 TCGAGTGGCT GGAAAAATCC TGGAGTCCCT GGACCGAGGG GTGAGCCCT
601 GTGAGGACTT TTACCAAGTTC TCCCTGTTGGG GCTGGATTTC GAGGAACCCC
651 CTGCCCCATG GGCCTCTCG CTGGAACACC TTCAACAGCC TCTGGGACCA
701 AAACCAAGGCC ATACTGAAGC ACCTGCTTGA AAACACCAC TTCAACTCCA
751 GCAGTGAAGC TGAGCAGAAC ACACAGCGCT TCTACCTATC TTGCCTACAG
801 GTGGAGCGCA TTGAGGAGCT GGGAGCCAG CCACTGAGAG ACCTCATTTA
851 GAAGATTGGT GTTGGAAACA TTACGGGGCC CTGGGACCAAG GACAACCTTA
901 TGGAGGTGTT GAAGGCAAGT GCAGGGACCT ACAGGGCCAC CCCATTCTTC
951 ACCGTCTACA TCAGTGGCGA CTCTAAGAGT TCCAACAGCA ATGTTATCCA
1001 GGTGGACCAG TCTGGGCTCT TTCTGCCCTC TCGGGATTAC TACTTAAACA
1051 GAACTGCCAA TGAGAAAATG CTCACTGCCCT ATCTGGATTAA CATGGAGGAA
1101 CTGGGGATGC TGCTGGGTGG CGGGCCCAACC TCCACGAGGG AGCAGATGCA
1151 GCAGGTGCTG GAGTTGGAGA TACAGCTGGC CAACATCACA GTGCCCGCAGG
1201 ACCAGCGGCG CGACGAGGAG AAGATCTACC ACAAGATGAG CATTTCGGAG
1251 CTGCAGGCTC TGGCGCCCTC CATGGACTGG CTTGAGTTCC TGTCTTCTT
1301 GCTGTCACCA TTGGAGTTGA GTGACTCTGA GCCTGTGGTG GTGTATGGGA
1351 TGGATTATTT GCAGCAGGTG TCAGAGCTCA TCAACCGCAC GGAACCAAGC
1401 ATCCTGAACA ATTACCTGAT CTGGAACCTG GTGCAAAAGA CAACCTCAAG
1451 CCTGGACCGA CGCTTGAGT CTGCACAAGA GAAGCTGCTG GAGACCCCT
1501 ATGGCACTAA GAAGTCCCTG GTGCCGAGGT GGCAAGACCTG CATCTCCAA
1551 ACGGATGACG CCCTTGGCTT TGCTTTGGGG TCCCTCTTCG TGAAGGCCAC
1601 GTTTGACCGG CAAAGCAAAG AAATTGCAAGA GGGGATGATC AGCGAAATCC
1651 GGACCGCATT TGAGGAGGCC CTGGGACAGC TGTTTGGAT GGATGAGAAG
1701 ACCCGCCAGG CAGCCAAGGA GAAAGCAGAT GCCATCTATG ATATGATTGG
1751 TTTCCCAGAC TTTATCCTGG AGCCCCAAGA GCTGGATGAT GTTTATGACG
1801 GGTACGAAAT TTCTGAAGAT TCTTTCTTC AAAACATGTT GAATTGTCAC
1851 AACTCTCTG CCAAGGTTAT GGCTGACCAAG CTCGGCAAGC CTCCCGCC
1901 AGACCAAGTGG AGCATGACCC CCCAGACAGT GAATGCCTAC TACCTTCCAA
1951 CTAAGAATGA GATCGCTTC CCCGCTGGCA TCCCTGCAGGC CCCCTTCTAT
2001 GCCCGCAACC ACCCCCAAGGC CCTGAACCTC GGTGGCATCG GTGTGGTCAT
2051 GGGCCATGAG TTGACCGATG CCTTTGATGA CCAAGGGCGC GAGTATGACA
2101 AAGAAGGAA CCTGCGGCC TGGTGGCAGA ATGAGTCCCT GGCAGCCTTC
2151 CGGAACCACA CGGCGCTGCAT GGAGGAACAG TACAATCAAT ACCAGGTCAA
2201 TGGGGAGAGG CTCAACGGCC GCCAGACGCT GGGGGAGAAC ATTGCTGACA
2251 ACGGGGGGCT GAAGGCTGCC TACAATGCTT ACAAAGCATG GCTGAGAAAG
2301 CATGGGGAGG AGCAGCAACT GCCAGCGTG GGGCTCACCA ACCACCAAGCT
2351 CTTCTCGTG GGATTTGCCCT AGGTGTGGTG CTCGGTCCGC ACACCAAGAGA
2401 GCTCTCACGA GGGGCTGGTG ACCGACCCCC ACAGCCCTGC CCGCTTCCGC
2451 GTGCTGGGCA CTCTCTCCAA CTCCCGTGAC TTCTGCGGC ACTTCGGCTG
2501 CCCTGTCGGC TCCCCCATGA ACCCAGGGCA GCTGTGTGAG GTGTGGTAGA
2551 CCTGGATCAG GGGAGAAATG CCCAGCTGTC ACCAGACCTG GGGCAGCTCT
2601 CCTGACAAAG CTGTTTGCTC TTGGGGTGGG AGGAAGCAA TGCAAGCTGG
2651 GCTGGGTCTA GTCCCTCCCC CCCACAGGTG ACATGAGTAC AGACCCCTCCT
2701 CAATCACCAC ATTGTGCCCT TGCTTTGGGG GTGCCCTGTC CTCCAGCAGA
2751 GCCCCCACCA TTCACTGTGA CATCTTTCCG TGTCACCCCTG CCTGGAAGAG
2801 GTCTGGGTGG GGAGGCCAGT TCCCCATAGGA AGGAGTCTGC CTCTTCTGTC
2851 CCCAGGCTCA CTCAGCCTGG CGGCCATGGG GCCTGCCGTG CCTGCCAAC
2901 TGTGACCCAC AGGCCTGGGT GGTGTACCTC CTGGACTTCT CCCCCAGGCTC
2951 ACTCAGTGCAG CACTTAGGGG TGGACTCAGC TCTGCTGTTGC TCACCCCTCAC
3001 GGGCTACCCC CACCTCACCC TGTGCTCCCT GTGCCACTGC TCCCAGTGCT

FIGURE 1A

DocID No.: CL001200-DIV II
 Serial No.: TO BE ASSIGNED
 Inventors: Ming-Hui WEI et al.
 Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

```

3051 GCTGCTGACC TTCACTGACA GCTCCTAGTG GAAGCCCAAG GGCCCTTGAA
3101 AGCCTCCTGC TGCCCCTGT TTCCCTGGGC TGAGAGGGGA AGTGCATATG
3151 TGTAGCGGGT ACTGGTTCCCT GTGTCTTAGG GCACAAGCCT TAGCAAATGA
3201 TTGATTCTCC CTGGACAAAG CAGGAAAGCA GATAGAGCAG GGAAAAGGAA
3251 GAACAGAGTT TATTTTACA GAAAAGAGGG TGGGAGGGTG TGGTCTTGGC
3301 CCTTATAGGA CCCTGTGCCA ATAAACAGAC ATGCATCCGT CAAAAAAA
3351 AAAAAAAAAA AAAAAAAAAA AAAAAAA (SEQ ID NO:1)
  
```

FEATURES:

5'UTR: 1-113
 Start Codon: 114
 Stop Codon: 2547
 3'UTR: 2550

Homologous proteins:

Top 10 BLAST Hits

		Score	E
CRA 18000005141003	/altid=gi 7662200 /def=ref NP_055508.1 KIAA...	1550	0.0
CRA 18000005084162	/altid=gi 2136744 /def=pir I46078 endotheli...	1430	0.0
CRA 18000005012182	/altid=gi 1706565 /def=sp Q10711 ECE2_BOVIN ...	1430	0.0
CRA 150000075554683	/altid=gi 9789315 /def=gb AAF98287.1 AF2302...	1027	0.0
CRA 1000682324124	/altid=gi 5821116 /def=dbj BAA83687.1 (AB031...	1001	0.0
CRA 108000024636251	/altid=gi 12721007 /def=ref XP_001827.2 en...	1001	0.0
CRA 18000004932659	/altid=gi 627989 /def=pir A53679 endothelin...	1000	0.0
CRA 18000005060029	/altid=gi 1706564 /def=sp P42893 ECE1_RAT EN...	996	0.0
CRA 18000005155376	/altid=gi 3287157 /def=emb CAA19767.1 (AL03...	995	0.0
CRA 18000004985166	/altid=gi 1082351 /def=pir JC2521 endotheli...	995	0.0

BLAST dbEST hits:

	Score	E
gi 6837875 /dataset=dbest /taxon=9606 /org=...	1094	0.0
gi 5925169 /dataset=dbest /taxon=9606 ...	983	0.0
gi 10725997 /dataset=dbest /taxon=96...	519	e-144
gi 2162041 /dataset=dbest /taxon=9606 ...	400	e-109

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|6837875 lung
 gi|5925169 amygdala
 gi|10725997 adrenal gland
 gi|2162041 total fetus

From tissue screening panels:

Hippocampus

FIGURE 1B

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Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

1 MNVALQELGA GSNMVEYKRA TLRDEDAPET PVEGGASPDA MEVGKGASPF
51 SPGPSPGMTP GTPRSSGLFW RVTCPHLRSI SGLCSRTMVG FQKGTRQLLG
101 SRTQLELVLA GASLLAALL LGCLVALGVQ YHRDPSHSTC LTEACIRVAG
151 KILESLDRGV SPCEDFYQFS CGGWIRRNPPL PDGRSRWNTF NSLWDQNQAI
201 LKHLENTTF NSSSEAEQKT QRFYLSCLQV ERIEELGAQP LRDLIEKIGG
251 WNITGPWDQD NFMEVLKAVA GTYRATPFFT VYISADSKSS NSNVIQVDQS
301 GLFLPSRDYY LNRTANEKVL TAYLDYMEEL GMLLGGRPTS TREQMQQVLE
351 LEIQLANITV PQDQRDRDEEK IYHKMSISEL QALAPSMDWL EFLSFLLSPL
401 ELSDSEPVVV YGMDYLQQVS ELINRTEPSI LNNYLIWNLV QKTTSSLDRR
451 FESAQEKLLE TLYGTTKKSCV PRWQTCISNT DDALGFALGS LFVKATFDRQ
501 SKEIAEGMIS EIRTAFEEAL GQLVWMDEKT RQAAKEKADA IYDMIGFPDF
551 ILEPKELDDV YDGYEISEDS FFQNMLNLYN FSAKVMADQL RKPPSRDQWS
601 MTPQTVNAYY LPTKNEIVFP AGILQAPFYA RNHPKALNFG GIGVVMGHEL
651 THAFDDQGRE YDKEGNLRPW WQNESLAAFR NHTACMEEQY NQYQVNNGERL
701 NGRQTLGENI ADNNGGLKAAY NAYKAWLRKH GEEQQLPAVG LTNHQLFFVG
751 FAQVWCsvrt PESSHEGLVT DPHSPARFRV LGTLSNSRDF LRHFGCPVGS
801 PMNPQQLCEV W (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 9

1	207-210	NTTF
2	211-214	NSSS
3	252-255	NITG
4	312-315	NRTA
5	357-360	NITV
6	424-427	NRTE
7	580-583	NFSA
8	673-676	NESL
9	681-684	NHTA

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

cAMP- and cGMP-dependent protein kinase phosphorylation site

18-21 KRAT

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 8

1	21-23	TLR
2	62-64	TPR
3	220-222	TQR
4	272-274	TYR
5	340-342	STR
6	465-467	TKK
7	582-584	SAK
8	757-759	SVR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 19

1	21-24	TLRD
2	30-33	TPVE
3	103-106	TQLE
4	161-164	SPCE

FIGURE 2A

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Inventors: Ming-Hui WEI et al.
Title : ISOLATED HUMAN ZINC METALLOPROTEASES...

5 192-195 SLWD
6 212-215 SSSE
7 214-217 SEAE
8 314-317 TANE
9 340-343 STRE
10 376-379 SISE
11 398-401 SPLE
12 403-406 SDSE
13 445-448 SSLD
14 453-456 SAQE
15 478-481 SNTD
16 514-517 TAFE
17 613-616 TKNE
18 705-708 TLGE
19 763-766 SSHE

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 4
1 365-372 RRDEEKIY
2 457-463 KLLETLY
3 535-542 KEKADAIY
4 555-561 KELDDVY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 14
1 9-14 GAGSNM
2 57-62 GMTPGT
3 61-66 GTPRSS
4 122-127 GCLVAL
5 159-164 GVSPCE
6 271-276 GTYRAT
7 331-336 GMLLGG
8 335-340 GGRPTS
9 464-469 GTKKSC
10 643-648 GVVMGH
11 714-719 GGLKAA
12 715-720 GLKAAY
13 782-787 GTLSNS
14 795-800 GCPVGS

[7] PDOC00047 PS00048 PROTAMINE_P1
Protamine P1 signature

776-787 ARFRVLGTLSNS

[8] PDOC00129 PS00142 ZINC_PROTEASE
Neutral zinc metallopeptidases, zinc-binding region signature

645-654 VMGHELTHAF

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	43	63	0.638	Putative
2	109	129	2.142	Certain
3	380	400	0.619	Putative
4	736	756	0.890	Putative

FIGURE 2B

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

BLAST Alignment to Top Hit:

>CRA|18000005141003 /altid=gi|7662200 /def=ref|NP_055508.1| KIAA0604
gene product [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=765
Length = 765

Score = 1550 bits (3969), Expect = 0.0
Identities = 765/811 (94%), Positives = 765/811 (94%), Gaps = 46/811 (5%)

Query: 1 MNVALQELGAGSNMVEYKRATLRDEDAPETPVVEGGASPDAMEVGKGASPFPSPGPGMTP 60
MNVALQELGAGSNMVEYKRATLRDEDAPETPVVEGGASPDAMEV
Sbjct: 1 MNVALQELGAGSNMVEYKRATLRDEDAPETPVVEGGASPDAMEV----- 43

Query: 61 GTPRSSGLFWRVTCPHLRSISGLCSRTMVGFQKGTRQLLGSRTQLELVLAGASLLLALL 120
GFQKGTRQLLGSRTQLELVLAGASLLLALL
Sbjct: 44 -----GFQKGTRQLLGSRTQLELVLAGASLLLALL 74

Query: 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNP 180
LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNP
Sbjct: 75 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNP 134

Query: 181 PDGRSRWNTFNSLWDQNQAILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQP 240
PDGRSRWNTFNSLWDQNQAILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQP
Sbjct: 135 PDGRSRWNTFNSLWDQNQAILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQP 194

Query: 241 LRDLIEKIGGWNIITGPWDQDNFMEVLKAVAGTYRATPFFTVDYISADSKSSNSNVIQVDQS 300
LRDLIEKIGGWNIITGPWDQDNFMEVLKAVAGTYRATPFFTVDYISADSKSSNSNVIQVDQS
Sbjct: 195 LRDLIEKIGGWNIITGPWDQDNFMEVLKAVAGTYRATPFFTVDYISADSKSSNSNVIQVDQS 254

Query: 301 GLFLPSRDYYLNRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLEIQLANITV 360
GLFLPSRDYYLNRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLEIQLANITV
Sbjct: 255 GLFLPSRDYYLNRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLEIQLANITV 314

Query: 361 PQDQRDRDEEKIYHKMSISELQALAPSMDWLEFLSFLLSPLLESDSEPVVVYGMDDYLQQVS 420
PQDQRDRDEEKIYHKMSISELQALAPSMDWLEFLSFLLSPLLESDSEPVVVYGMDDYLQQVS
Sbjct: 315 PQDQRDRDEEKIYHKMSISELQALAPSMDWLEFLSFLLSPLLESDSEPVVVYGMDDYLQQVS 374

Query: 421 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTTKSCVPRWQTCISNT 480
ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTTKSCVPRWQTCISNT
Sbjct: 375 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTTKSCVPRWQTCISNT 434

Query: 481 DDALGFALGSLFVKATFDROSKEIAEGMISEIRTAFFEEALGQLVWMDEKTRQAACEKADA 540
DDALGFALGSLFVKATFDROSKEIAEGMISEIRTAFFEEALGQLVWMDEKTRQAACEKADA
Sbjct: 435 DDALGFALGSLFVKATFDROSKEIAEGMISEIRTAFFEEALGQLVWMDEKTRQAACEKADA 494

Query: 541 IYDMIGFPDFFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWS 600
IYDMIGFPDFFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWS
Sbjct: 495 IYDMIGFPDFFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWS 554

Query: 601 MTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGIGVVMGHELTHAFDDQGRE 660
MTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGIGVVMGHELTHAFDDQGRE
Sbjct: 555 MTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGIGVVMGHELTHAFDDQGRE 614

Query: 661 YDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQTLGENIADNGLKAAY 720
YDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQTLGENIADNGLKAAY
Sbjct: 615 YDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQTLGENIADNGLKAAY 674

FIGURE 2C

Docket No.: CL001200-DIV II
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Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

Query: 721 NAYKAWLRKHGEEQQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARFRV 780
NAYKAWLRKHGEEQQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARFRV
Sbjct: 675 NAYKAWLRKHGEEQQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARFRV 734

Query: 781 LGTLSNSRDFLRFHGCPVGSPMNPGQLCEVV 811
LGTLSNSRDFLRFHGCPVGSPMNPGQLCEVV
Sbjct: 735 LGTLSNSRDFLRFHGCPVGSPMNPGQLCEVV 765 (SEQ ID NO:4)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
CE00310	E00310 neutral_endopeptidase	456.3	2.6e-133	1
PF01431	Peptidase family M13	270.4	2.4e-77	1
CE00339	E00339 vitamin_D_receptor	4.3	1.1	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00339	1/1	367	398 ..	412	443 .]	4.3	1.1
PF01431	1/1	607	810 ..	1	225 []	270.4	2.4e-77
CE00310	1/1	140	811 .]	66	798 .]	456.3	2.6e-133

FIGURE 2D

1 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
51 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
1001 NNNNNNNNNN NNNNNNCACC TTAGACTTGA CAGGCCTGCT
1051 TAGTCGGACT CTAAAGCACC CCTTTGCTTT TCGTTAAATA TTGCTTGCTG
1101 TTAGTTTTT TTCTCCTTGT AAATCTCCA AATAAACCGG TTTGCTTTC
1151 CCAAGTTAGA AGTGTAGCA CGTCTTTCT TAAATATCT GTGCATGGCT
1201 GTTTTTTCC CTGCCATT GTCACCATCT GTAACCCCTCC CTTTATGAGA
1251 CGATCTGATG ACAGCAGTTA TCTTGGAGAG TAGAAGTGTG GTCTTGAGC
1301 GCCATGGAAG AGTAGAGTC GTGTATGCTG TGTGTGTGTG GAGTGTATGC
1351 TCCCCCTGCA CTTGGTGTGT GTACATACAG AACACAGTG TGCGTGTGTG
1401 TTGGCTCTGG GTGTGTGTG CGTGTGTACA CTGTGTGTG GTATGAGTG
1451 TGTGTACATT CTGTGGGCAT CTCGTGTGTG TGTGGACTGTG GTGCTGGCG
1501 TCGTGCCTGC CCGTGTCTT GGCGCCTTGG CGTCTATGCG TTCTCTGCAC
1551 ATAGGTAGGT ACCACGTGCA CACCTGAAT GTGAGTGAAC TGCGTGTGTG
1601 CTATGTATTT GCCGGCTGAA GAGGGGCTGT GTGGACTACT GGGGAAAGAC
1651 GTTCCCTCANG AGGGCATAAT TTCTCTAAAG TGCTTAAAGG GGATGGAGAG
1701 AGCCTGAAAT TTGGGGGAAG TAGGCCAAGG AGTATTATCA ACGTCTGGC
1751 CTGGTTGAAT TTCATTACTT TTCCTAGGAA AGTAAATTAT GGGTGGCTTG
1801 AAGGAGGGTG CTGCTGAGAT GGGGGCGGA CCATGAAGCG TGGAGGGTC
1851 TCCGGTGTG CTGGAGGGCA GCTGGAGCCT GCGGAGAGCC TCGGCGCGCT
1901 CCTCCCTCTC CCCCACCCCTC CCCCCACCCC GGGCGGGGCT CCGCGTGGGG
1951 CGGTGGACTC GGGGGGGGG GGGGGGGGCC GCGGCGGAGC GGGGGTGTG
2001 CGCGGCGGCC GTGATGGCTG GTGACGGCGG GGGCGGCCAG GGGACCGGGG
2051 CGCGGGCCCG GGAGCGGGCC AGCTGCGGGG AGCCCTGAAT CACCGCCCTGG
2101 CCCGACTCCA CCATGAACGT CGCGCTGCAG GAGCTGGAG CTGGCAGCAA
2151 CGTGAGTGGG GGGGGGGGGC TCCACGGGAG GGGACTGGGT GGAGGGGGAC
2201 GAGGCAGAGG GTCGGCCGC GGAGGGGCAG CGGGTGGCCCG GCTCGCGGAG
2251 GTAAGGCTGC CTCCCCGGGC TGGTGGAGGG GTGATAGAGA GACCCCGGGC
2301 CCGAGAGCAG GGCAGGTGGG AAGGGAAGGG CCCTCTTAGC AGGGCGGAGG
2351 GGTCCCGCAG GCAGGGGAGCA CTGGGGCAGG GTCTGGGGCA AATAGCCCTC
2401 TCTGCCTGAC CTCGGTTGGC AACCCCGACT GTCTGGCAGA TGGTGGAGTA
2451 CAAACGGGCC ACGCTTCGGG ATGAAGACGC ACCCGAGACC CCCGTAGAGG
2501 GCGGGGCCTC CCGGAGGCC ATGGAGGTGG GCAAGGGGGC TTCCCCCTTC
2551 TCACCCAGGCC CCAGCCCTGG CATGACGCC GGCACACCCA GGAGCTCTGG
2601 GCTGTTCTGG AGGGTCATCT GCCCCCACCT CCGCTCCATC TCTGGCCTCT
2651 GCTCTAGGAC TATGGTGAGG CGATGCTAAG CGGTGACGTT GCACAAAACA
2701 GACTCAAGGC TCAACTCACT GGCTGGCCTC ATTGCCCCCG GGCCCAGAGT
2751 TAACCCCTGTG GCTCTGAAAA CTGCGCTGTGG CTTCACCCCTC TGGTAATCTT
2801 GGATCCCTGC CCTGCATCTC AGTCACTCTC TGTCCCCCTG TGTTCCCCAG
2851 GTGGGATTCC AGAAGGGGAC AAGACAGCTG TTAGGCTCAC GCACGCAGCT
2901 GGAGCTGGTC TTAGCAGGTG CCTCTCTACT GCTGGCTGCA CTGCTTCTGG
2951 GCTGCCTTGT GGCCCTAGGG GTCCAGTACC ACAGAGGTAG GTGGGCCAC
3001 ACTCTTCGTC AGTATTCTATA ACTAGGGTT CTGGAGGCCT AAGGGCCTCT

FIGURE 3A

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3051 AAGATTTCA CTTGTGGAA CCAAGCCTTC CCTGCAGAAA AGCCCCCGGC
3101 TTTGCTTCT CTTCCAACC TTCCCTGCTGT CATGGCCCTT GCAGAGTTG
3151 CCTCTTCCAG ACAGACAGAC TGACAGTCTC CTACCCCTCCG GCCATGTTCC
3201 CTACCACAGA CCCATCCCAC AGCACCTGCC TTACAGAGGC CTGCATTGCA
3251 GTGGCTGGAA AAATCCTGGA GTCCCTGGAC CGAGGGGTGA GCCCCCTGTGA
3301 GGACTTTAC CAGTTCTCCT GTGNNNNNNN NNNNNNNNNN NNNNNNNNNN
3351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
3401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
3451 NNNNNNNNNC TTAGCAAATA GGCAGTGTCC CATGAATGAG GAAGTGGATG
3501 GTTCTGTGAA CACTCCCAGA GGGTGgggAG GCAGAGAGCA GGGGACTATT
3551 GAGAACTGCA GATGGGTTTG ATGGGGCAG AACTCTGGT ACAATGGAGG
3601 GCCGCTTCTC TGCACTCTGT TTGGAGCACT GTCTGGGTGT GGTAGACACC
3651 AGGGAGCCTG TACTGCTTAG ATATCCTTGG GTCTCCATGG ACAGGGAGAG
3701 GAAGGCCACGG CTGCTGTTT CAGACACTC TCCTGGGTCT GCGTTAGCAG
3751 GACTGCTCAT TGACAAGGCA AGGAGAGAAA CCGAGCAAGG GCCAGGGACT
3801 CCCCTTCAGC AGTTAACGTA ATTGCCACCT GGATCCTGTG TTCTGCCCCA
3851 CAGAAAACAC CACCTTCAAC TCCAGCAGTG AAAGCTGAGCA GAAGACACAG
3901 CGCTTCTACC TATCTTGCTT ACAGGTGGAG CGCATTGAGG AGCTGGGAGC
3951 CCAGCCACTG AGAGACCTCA TTGAGAAGGT AGGGCCACTG AGCCGGTTGA
4001 GGGCAGGGGA GCAGGAGAGG CTTTGAGAGA GGAGATGGCC CAGGAACGCT
4051 TTGGGAGCTC CTGCACTAAT CATTCCACTT ATGGTCTCTA CATAGATTGG
4101 TGGTGGAAC ATTACGGGGC CCTGGGACCA GGACAACCTT ATGGAGGTGT
4151 TGAAGGCAGT AGCAGGGACC TACAGGGCCA CCCCATTCTT CACCGTCTAC
4201 ATCACTGCGC ACTCTAACAG TTCCAACAGC AATGTTATCC AGGTGATGAG
4251 CTGGAAAGG GTGGGGAGAG ACTTACGGGAC ACTTTGCTGA GCCCAGACTT
4301 CCCTCTCCTG TGACAGGGCAG GCTGGGCTGA CCCCCCGGCC CCACCCCTAC
4351 CCCCGCTCGG GAATTCAAGGT TCCCATGGTG GGGAAAGCGA GGGGCTCACC
4401 TCCTTCTCTT GACATTGCGAG GTGGACCAGT CTGGGCTCTT TCTGCCCTCT
4451 CGGGATTACT ACTTAAACAC AACTGCCAAT GAGAAAGTAA GGAACATCTT
4501 CCGAACCCCC ATCCCTACCC CTGGCTGAGC TGGGCTGATC CCTGTTGACT
4551 TTTCCCTTTG CCAAGGTCA GAGCAGGGAA GGTGAGCCTA TCCTGTCACC
4601 TAGTGAACAA ACTGCCCTC CTTTCTTTCT TCTTTCTTC CTCCCTCCCT
4651 CCCTTCTTC CCCTTTCTTCC TCCCTCCTTC CTCTTATTCT TCTAGTAGGT
4701 TTCATAGACA CCTACTGTGT GCCAGGTCCA GTGGGGGAAT TCTGAGATAT
4751 AAGTTTNCAG AGCCCATTG CAGCAGGAGA GGGGATCCTT TAGAGTCGCA
4801 CAAACAGGTC AGTCAAGTCT AAAGACNNNN NNNNNNNNNN NNNNNNNNNN
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5201 CCGACTCAAA AAAAAAAA AAAAGAAAG AAAAGAAAG AAGGAACAGT
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5301 CCCGCACTTT GGGAGGCTGA GGCGGCGGA TCACTTGAGG TTAGGAGTTC
5351 AAGACCAGGC TGGCTACAA GGTGAAAACC CGTCTCTACT AAAAATACAA
5401 AAATTAGCCA GGCATGGTGG TGTGCACCTG TAATCTCAGC TACTTGGGAG
5451 GCTGAGGCAA AGAGAATCGC TTGAATCCAG GAGGCAGAGG TTGCAGTGAG
5501 CTGAGATGGC ACCACTGCAAC TCCAGCCTGG GCAACAGAAC AAGACTTCAT
5551 CTCAAAAAAA AAAAAAAAAG TGTTGACGAG GGGAAAGGCTA GGTGTGCTG
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5651 AGAGGCTGGA GAGGTGGGCA GGAATGGGTT ATGGAGGGGA CCTTGAATAG
5701 CACACTACGG AGTTTATTCT GTAGCTCCCG GAGAGCCATT GCATGCTCCA
5751 AAGTAGGGAG GGAGCGCANT GCTTTGGAA GTCACTTGT TTGGGGTGTG
5801 AAGAGTANAT GTGAGAACNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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6001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
6051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3B

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

FIGURE 3C

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
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9151 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
9201 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
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9301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
9351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
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10501 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
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11251 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
11301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
11351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
11401 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNAG TTCCAGGCC
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11501 AAAAGATGTA AGCCTGGCA TAGGTGGCCG GGTGCCGTT TGTCGCCAC
11551 GCTATCTTGG GGAGGGATT AAGGCAAGGA AAATTCACCT TGAGGCCAA
11601 GGAAGGCACA AGGGTTATCA CGTGAAGCCG AGGATCACCA TCACCATGCA
11651 CTAACACGCC TTGGGCAAGC ACGAAGCGAG GAGTTGCCAT CTCAAAACAA
11701 AAACAAAAA CAAACAAACA AAATGTAAT CAACTGTAT TGGTAAGGCT
11751 TCTGGTCAAC AGTATGCTGT CAATAGTTAA GTTTTGGGC TGGCGCAGT
11801 GGCTCACGCC TGTATCCCC GCACTTGGG AGGCCAAAGC GGGTAGATCA
11851 CCTGAGGTCA GGAGTCGAGA CTAGCCTGGC CAACATGGCG AAACCCAGTC
11901 TCTACTAAAAT ATATAAAAAT TAGCCAGCG TGTTGGTGGG CACTTGTAAAT
11951 CCCAGCTACT CAGGAAGCTG AGGCAGAACT GCTTGAACTG GGAAGTGGAG
12001 GTTGCAGTGA GCCGAGATCG TGCCATTGCA TTCCAGCCTG GGCGACAAGA
12051 GCAAAACTCC ATCTCAAAA AAAAAAAA AAAAAAAGTT GTTTTGGGG
12101 AGTCAAAAAT GAGGCCAGGC GCAGTGGCTC ATGCCTGTAA TCACAGCACT
12151 TTGGGAGGCC GAGGCCGGGT GATCACCTGA GGTCAAGGAGT TCGTGACCAG

FIGURE 3D

12201 CTTGGCCAAC CTGGTAAAC CCCGTCCTCA CTAAAAATAC AAAAATTAGC
12251 CGGGCATGGT GGCGGGCGCC CGTAATCTCA GCTACTTGGG CGGCTGAGGC
12301 AGGAGAATTG CTTCAACCCG GGAGGCAGAG GTTGCAATGA GCTGAGATCG
12351 CGCCACTGCA CTCCAGCCTT GGCGACAGAG GGAGACTCCA TGTCAAATTA
12401 AAAAAAAAGAC CCCAGGATT TGGACTGTGC AGGGGTCGGT GCCCCAAACC
12451 CCCACGTTGT TCAAGGTCAA CTGTACACTG TCATAGTCGG GAAAACCTCA
12501 TCACTGCAGC TGCTCCCTGT TCTTGAAACC TGAAGCGGGG AACTGGATCC
12551 TGGGACACTA CTGCCCTCTA TCGCCTGTG GTCTCAAAG AAATAATCCC
12601 TTCAATTTCG CAAGGCCTGT GGTGTCATTC CCTTTAACAA GATAAGGAAA
12651 CCGAGGCCAG GACGTGGTGG AAAATAATCA AGGTCACACA TCTATGTCA
12701 AAAGTGGAGT ACAACCCAG GCTCCTCATT CCCAGGTCAAG TCCAGTGACC
12751 TCAATTGACA TGAAATGTGT GAGGTCCCTC TGTCGGCCCTG TGGCAGGGCC
12801 TGAAGAGGAC AGCGTATGTA AATCAAGTCT TGTCCTCTCA TGAGTGAGGC
12851 AGAGTAGAAA ATAACAGTAA TTCACTAGGA CCGAATCTGC ATTGTAAACA
12901 GAGAGGAAAG GGCTAGTATT TGGCAGAAGG ATGTCAGGA ACATTTAGA
12951 GATAAGAGGT GACATTTGGG TTCTGAGGGG TGAGTAGGGG TGTGCCAGGG
13001 TGCAAAAGGT GAAAAGACAG CTCTAGCAGC TGTTAAGGGC TAAGGGCAT
13051 GGAGAAACAG CAAGACTTTG GGGAACTGGT AGAATTCTAA TTCTGGAAAA
13101 TTTGAACAAG GTAATTTCGTT GTGTGTGGTT AAGGTATTAC ATACATACAG
13151 TAAAATAAAA TGCAATAGTT GCTGGGTGTG GAGGCTCACG CCTGTTAATC
13201 CCAGTACTTT GGAAGGCAGA GGCGGGTGGA TCATCTGAAG GTCAGGAGTT
13251 CGAGACCAGC CTGACCAACA TGGTAAAAC CCGTCTCTAC TAAAATACA
13301 AAAATTACCT GGGTGTGGTG GCAGGGCGCC GTAATCCCAG CTACTTGGGA
13351 GGCTAAGGGG GAAGAATAGC TTGAAACCCG GAGGTGGAGG TTGCAGTGAG
13401 CTGAGATTGC ACTATTGCCG TCCAGCCTGG TGACAAGAG TGAAAAGCTG
13451 TCTCAAAATA AAATAAAAAT GTAATAGTCT AATTGATTTT TTTAAAAAAT
13501 GTAGACATCC ACGTATCTAC CACCTAGGT AAGATACTAG AGATTCCAGC
13551 AACCTGGGAG GATCCCTCGT GCCCCTTCA GGTCTATATG AGCCTCCACC
13601 GTTCCCCAGT CCCCTGGAAG GAGAGGGGT GGGAGAGGCA ACATGAAACC
13651 TAAAAACCAG TGGGCTTCGC GCCTGTAATC CCAGCTATTG GGTTGGCTGA
13701 GGCAGGAGGA TCACTTGCC AGGAGTTGGA GGCTGCAGTG AGCTATGATC
13751 GCGCCACCAGC ACTCCAGCCT GGGCGACAGA TCAAGACCCC ATCTCTAAC
13801 AAACAAACAA ATAAACACCC CTCAAAACCC ATGGCTTCAG GCCTGGCGC
13851 GTAGCTTACT TCTGTAATCT CAGCACTTTG GGAGGCCAG GAGGGCGGAT
13901 CACTTGAGGT CAGGAGTTCC AGACCAAGACT GGCACACATG GCGAAACCCC
13951 GTCTCTACTA AAAATAAAA AAAAAGAAAA ATTGGCCGGG CGCGGTGGCT
14001 CACACCTGTA ATTACCAAGCA GNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14051 NNNNNNNNNNN NNNNNNNNNNN NTTTTAAAGA ATGAGACAT CCACGTATCT
14101 ACCACCTAGG TAGAGATACT AGAGATTCGA GCAACCTGGG AGGATCCCTC
14151 GTGCGCCTTT CAGGTCTATA TGAGCTCTCA CGGTTCCCCA GTCCCCCTGGA
14201 AGGAGAGGGG GTGGGAGAGG CAACATGAAA CCTAAAAAACC AGTGGGCTTC
14251 GCGCCTGTAA TCCCAGCTAT TGGGTTGGCT GAGGCAGGAG GATCACTTGC
14301 CCAGGAGTTG GAGGCTGCAG TGAGCTATGA TCGCGCCACC GCACTCCAGC
14351 CTGGCGACA GATCAAGACC CCATCTCTAA GCAAACAAAC AAATAAACAC
14401 CCCTCAAAAC CCATGGCTTC AGGCCTGGCG CGTAGCTTA CTTCTGTAAT
14451 CTCAGCACTT TGGGAGGTCA AGGTGGCGG ATCACTTGAA GTAAGGAGTT
14501 CAAGTACCAT CCTGGCTAAC ACGGTAAAC CCCGTCCTCA CTGAAAAGAC
14551 AAAAATTTA GCCGGGCGTG GTGGGGCGC CCTTTAGTCT CAGCTACTCG
14601 GGAGGCTGAG GCAGGAGAAAT GGCGTGAACC CGGGAGGTGG AGCTTGAGT
14651 GAGCTGAGAT CGCACCACTG CACTCCAGTC TGGGTGACAG AGTGAGACTC
14701 CATCTAAAAA AAAAAAAAGA AGAAGTCAAA GTAGTAGAAA CTGCTGATAG
14751 ACTGAATGTG GGGGGTTAGG GAGATGGAGG AAGCTGAGTG ACTCCCAGGT
14801 TTCTTGATG TGTTGACTGAC TGGATATAAA ATTAGTTGTG GGCCGGGCAC
14851 GGTGGCTCAT GCCTTTAAC CCAAGCACTT GGGAGGCCAA AGCGGGCAGA
14901 TCACTTGAGC TCAGGAGTTA AAGACCAGCC TGGGAAACAT GGTGAGACCC
14951 CTTCTGTAAG GGNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
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15051 AGTTATTGGG AGTCTACAAG ATTCTTCAC ACTATGCCCT CAAAATTGAC
15101 TGTTCATGTA TGTGCAGACA TATAGAAAAA CAACGGGAGC CAGGCGCGGT
15151 GGCTCACGCC GGTAAATCCCA GCACTTTGGG AGGCCAAGGC GGGTGAATCA
15201 TGGGGTCAGG AGTTGAGAC CAGCCTGGCC AACATGGTGA AACCTGGTCT

FIGURE 3E

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

15251 CTACTAAAAA TACAAAAAAAT TAGCCGGCG TGTTGGCGGG TGTCTGTAAT
15301 CCCAGCTACT TGGGAGGCTG AGGCAGGAGA ATCACTTGAA CCCAGGAGC
15351 GGAGGTTGCA GTGAGGCCAG ATCGGCCAG TGCACCTCAG CCTGGGCAGC
15401 AGAGCAAAAC TCTGTCTCAA AAAAAAAAAGA AAAAAAAAGA AAAGAAAAGA
15451 AAAACAACTG GATGTAAATT GATGAACAAA TGAAGTAGTG CTGCTTGGG
15501 CAGTGGGATT ATAAGAGTCC TTAAAGTTG TCTATGTGTT TATGTTAAC
15551 TATATAACTA GAAGAAATAT TTATTATTA GGATATGATA ATGGATGTGC
15601 TTAAAGTATT ACCTGTAAAGG ATGTTATGG TTTTTATGGC AATGTTGTTT
15651 ATAATAGCAG AAAATGAGAA CAGGTTAAAT GTCCAACCTAT AGGGTAAAGG
15701 AAAAATAAAAT TGTTGGTTAGG ATGGGGTGTG AGGATCCTTA AATGGCTGAT
15751 ATATCTTCA GCAAAAAAAAG TAGGTTACAA AAAATATATA CCCTATACAA
15801 CATAATTCCA TATTTTATAT GCATATCAGG GGAGGGAAAA ACTCTAGAAG
15851 TGGGTAAATCA AAATGTAAA AGAACTTATC TATGAATGAG TGCTTTATAA
15901 CTGGTCTGTT CTTCAATTCT CAATTTCCTA AATTTCTGT GAATGTCCTC
15951 TTTTCATAAT CAGATAAAA TCATTGCACT AGGCTGGCG TGTTGGTCA
16001 CGCTTGTAAAT CCCAGCACTT TGGGAGGCTG AGGCAGGGTGG ATCACGTGGT
16051 CAGGAGTTCA AGACCAACCT GGCAAGATG GTGAAACCCCC AGCTCTACTA
16101 AAAATACAAA ATTACCCGG GCATGATGGC GGGAGCCTGT AATCCTAGCT
16151 ACTTGGGAGG CTGAGGCAGG AGAATCGCTT GAACTCGGGA GGCAGGAGTT
16201 GCAGTGAGCC GAGATTGCGC CACTGCACTC CATCCTAGGT AACACAGCCA
16251 GACTCTGTCT CAAAAAAATCAT TGCACATATAT TAAATTATAA
16301 TATAATTGTA TGAACTTATT GTCAATTAAA ATGTTGACTT AATTAAGAAA
16351 AAAGCCAGCC ACAATCCCAG TACCTTACA AATGGTGTGTT CCTTCTCATC
16401 GTCTCCAGGT GCTCAGCCGT ATTTCTTAG TCTAGACGTT CCCATTTCCC
16451 CTGGGTGGAC AGGGATGGGG CACCAAGGGT GGATGGGTGG GGCAGGGATG
16501 CATTCACTGC AGGGGAAGGC TGACTTTACC TCCTCCCTCC CAGGCAGAGG
16551 GGATGATCAG CGAAATCCGG ACCGCATTG AGGAGGCCCT GGGACAGCTG
16601 GTTTGGATGG ATGAGAAAGAC CCGCCAGGCA GCCAAGGAGA AAGTGAGCGG
16651 TGGCTAGGGT TGGGGCGCCA TCTTGAGGTG GGTTCAAGG ATACAGTTT
16701 GCTAGGAACC TGGGGAGGA AACAAACCC TAACTGGTC TCTTCAGGCA
16751 GATGCCATCT ATGATATGAT TGGTTCCCA GACTTTATCC TGGAGCCCAA
16801 AGAGCTGGAT GATGTTTATG ACGGGGTGG TACCTACGCT CATCAGTACT
16851 GAACTTCAGC CCTGTAGAGG GCACTGTTCC CTGGGCTTAG AAATTGGGC
16901 TCAAGCACTG GGAAAGAGGT GCTTGTGGT TTCTTTAGA GGCAGATGGA
16951 GGTAACCCAGC ATTGTTAAA TGTTGGCTCT GTGACAGGCT GCAGGCCAA
17001 CAGCACTGAA ATATAGTGT AACGAGCCAA GATTGGAGT CAAGCCTAAT
17051 CAAATTCTGT TTCTACCTC AACTTTGTAA CCTTAACAAA ATCTCTCTAG
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17151 TAGGTTGGTT GTGAGATAAA TGAATACAGT ATGAAAAAAA ACAGCACCCA
17201 TAACATAAAAT GGCTTTAAA TATTGCCAAT TATGGTTTAC TAGATATTT
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17901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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18201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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FIGURE 3F

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

18301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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18501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
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18951 CGTCACCCC AGAGAGTGAA GGGGGCCCC CCCGCCCAA AGGAAAGGGG
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19051 CCCCCCGGG GAGAACCTT GGATGGGCT CANCCCCCCC TCTTTTTTT
19101 TCCCCCGAAA ACCCCCCCCAAAAGTTTT TTAAAAAAAC AAAAAGGGG
19151 GGTTGGTTT TTTGGGCCCC GTGGCCCTT TGTTTAAAT TGGGAGAAAG
19201 AGGGCTAAA GGGGGGATTG AAGAAAAAAC CCCCCCCCAA TTGCCCCAAA
19251 TTGTAATTTC CTAACCCCAA AAGGGCCCC TAAAATTTC GGGAAACCC
19301 GTGTGGCAA TGGCCCATTA GTTACCCAA TGCCCTTATT GACAAAGTA
19351 GGGCCCCATG GAGTCGTCCC CTCTAGCCTA GAATTCCAG TGGCTCCTGC
19401 AAGGGCCTTG GGACATTGAT GTAGCCCCAA GGGCCCTGAA GTCTGTGGAC
19451 CAGGGCTGGT GGGGCACTGC TGCCCCAAG AGACGAGCTC TGGTTTTGGT
19501 GGGGTGCAAAG GGTGAGTTCT CCTCAGGGCG CGAGTATGAC AAAGAAGGGA
19551 ACTGCGGCC TGGTGGCAGA ATGAGTCCTT GGCAGCCTTC CGGAACCACA
19601 CGGCCTGCAT GGAGGAACAG TACAATCAAT ACCAGGTCAA TGGGGAGAGG

(SEQ ID NO:3)

FEATURES:

Start: 2113
Exon: 2113-2151
Intron: 2152-2439
Exon: 2440-2664
Intron: 2665-2850
Exon: 2851-2986
Intron: 2987-3209
Exon: 3210-3320
Intron: 3321-3519
Exon: 3520-3636
Intron: 3637-3853
Exon: 3854-3978
Intron: 3979-4095
Exon: 4096-4242
Intron: 4243-4420
Exon: 4421-4486
Intron: 4487-4576
Exon: 4577-4581
Intron: 4582-4707
Exon: 4708-4811
Intron: 4812-5525
Exon: 5526-5591
Intron: 5592-11594
Exon: 11595-11742
Intron: 11743-13150
Exon: 13151-13240
Intron: 13241-16408
Exon: 16409-16642
Intron: 16643-16747
Exon: 16748-16825
Intron: 16826-18962

FIGURE 3G

Docket No.: CL001200-DIV II
 Serial No.: TO BE ASSIGNED
 Inventors: Ming-Hui WEI et al.
 Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

Exon: 18963-19222
 Intron: 19223-19321
 Exon: 19322-19347
 Intron: 19348-19526
 Exon: 19527-19647

CHROMOSOME MAP POSITION:
 Chromosome # 3

ALLELIC VARIANTS (SNPs):

DNA			Domain	Protein		
Position	Major	Minor		Position	Major	Minor
2707	A	G	Intron			
4209	C	T	Exon	289	S	S
4355	-	T G	Intron			
15455	-	A C	Intron			

Context:

DNA
Position

2707	TGACCTCGTTGGCAACCCGACTGTCTGGCAGATGGTGGAGTACAAACGGGCCACGCTT CGGGATGAAGACGCACCCGAGACCCCCGTAGAGGGCGGGCCTCCCCGACGCCATGGAG GTGGGCAAGGGGGCTTCCCCTTCTACCAGGCCAGCCCTGGCATGACGCCCTGGCAC CCCAGGAGCTCTGGCTGTTCTGGAGGGTCATCTGCCACCTCCGCTCCATCTCTGGC CTCTGCTCTAGGACTATGGTGAGGCGATGCTAAGCCGTGACGTTGCACAAAACAGACTCA [A, G] GGCTCAACTCACTGGCTGGCCTCATTGCCCGGGCCCAGAGTTAACCTGTGGCTCTGA AAACTGCCCTGTGGCTTCACCCCTCTGTAATCTTGGATCCCTGCCCTGCATCTCAGTCACT CTCTGTCCTCTGTGTTCCCCAGGTGGGATTCAGAAGGGGACAAGACAGCTGTTAGGCT CACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCCTCTACTGCTGGCTGCACTGCTTC TGGGCTGCCCTGTGGCCCTAGGGGTCCAGTACCAACAGAGTAGGTGGGCCACACTCTTC
4209	CCTATCTGCCTACAGGTGGAGGCATTGAGGAGCTGGGAGCCAGCCACTGAGAGACCT CATTGAGAAGGTAGGCCACTGAGCCGGTTGAGGGCAGGGGAGCAGGAGAGGCCCTGAGA GAGGAGATGGCCAGGAACGCTTGGGAGCTCCTGCACTAATCATTCCACTTATGGTCTC TACATAGATTGGTGGTGGAACATTACGGGCCCTGGGACCAGGACAACTTATGGAGGT GTTGAAGGCAGTAGCAGGGACCTACAGGCCACCCATTCTCACCGTCTACATCAGTGC [C, T] GACTCTAAGAGTTCAAACAGCAATGTTATCCAGGTGATGAGCTGGGAAAGGGTGGGAGA GACTTAGGGACACTTGTGAGGCCAGACTTCCCTCTCTGTGACAGGCAGGCTGGCTG ACCCCCCGGCCCCACCCCTACCCCGCTCGGAATTCAAGGTCCCCTGGTGGGAAAGCG AGGGGCTCACCTCTTGTGACATTGCAAGGTGGACCAGTCTGGCTCTTCTGCCCTC TCAGGGATTACTACTAAACAGAACTGCCAATGAGAAAGTAAGGAACATCTTCCGAACCC
4355	GAGCTCCTGCACTAATCATTCCACTTATGGTCTCTACATAGATTGGTGGTTGAAACATTA CGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACA GGGCCACCCATTCTCACCGTCTACATCAGTGGCAGCTAAGAGTTCCAACAGCAATG TTATCCAGGTGATGAGCTGGGAAAGGGTGGGAGAGACTTGGGACACTTGTGAGGCC AGACTTCCCTCTCTGTGACAGGCAGGCTGGCTGACCCCCCGCCCCACCCCTACCC [-, T, G] CTCGGGAATTCAAGGTCCCCATGGTGGGAAAGCGAGGGGCTCACCTCCTTCTGACAT TGCAAGGTGGACCAGCTGGGCTCTTCTGCCCTCTCGGGATTACTACTAAACAGAACTG CCAATGAGAAAGTAAGGAACATCTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGG TGATCCCTGTGACTTTCCCTTGCAAGGGTCAGAGCAGGGAAAGGTGAGCCTATCCTG TCACCTAGTGAACAAACTGCCCTCCCTTCTTCTTCTCCCTCCCTCCCT

FIGURE 3H

Docket No.: CL001200-DIV II
Serial No.: TO BE ASSIGNED
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ZINC METALLOPROTEASES...

15455

CACGCCGGTAATCCCAGCACTTGGGAGGCCAAGGCAGGTGAATCATGGGTCAGGAGTT
CGAGACCAGCCTGGCCAACATGGTAAACCTGGTCTCTACTAAAAATACAAAAATTAGC
CGGGCGTGGTGGCGGGTGTCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACATCA
CTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCGGCCAGTGCACCTCCAGCCTG
GGCGACAGAGCAAACACTGTCTCAAAAAAAAAAAAAAGAAAAGAAAAGAAAA
[-, A, C]
AACTGGATGTAAATTGATGAACAAATGAAGTAGTGCTGCTTGGCAGTGGGATTATAAG
AGTCCTTAAAGTTCTATGTGTTATGTTAACTATATAACTAGAAGAAATATTATT
TATTAGGATATGATAATGGATGTGCTTAAAGTATTACCTGTAAGGATGTTATGGTTTT
ATGGCAATGTTGTTATAATAGCAGAAAATGAGAACAGGTTAAATGTCCAACTAGGGT
AAAGGAAAAATAAATTGTGGTTAGGATGGGTTGTGAGGATCCTTAAATGGCTGATATATC

FIGURE 3I